

IDENTIFICATION

Species: *Prunus persica*

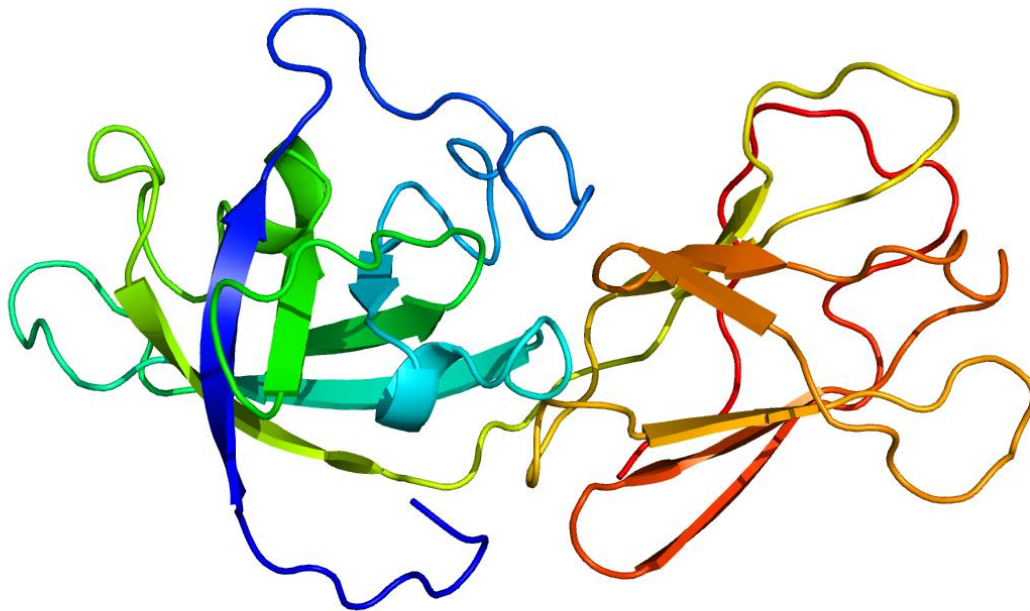
Locus: Prupe.1G516600

Gene Model: Prupe.1G516600.1.p

Description: PrpEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

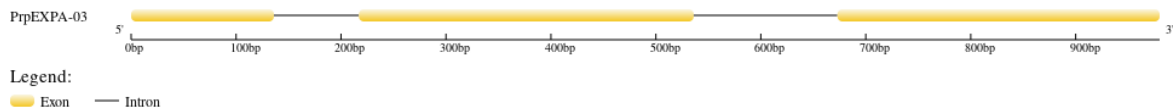
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1

KEGG: <https://www.genome.jp/entry/gn:T03092>

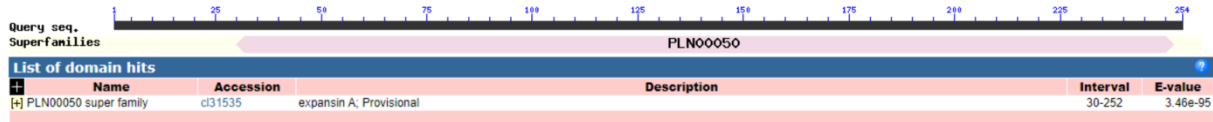
EXTERNAL RESOURCES

https://www.rosaceae.org/species/prunus_persica/genome_v2.0.a1

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PrpEXPA-03

MLGSLLLFLLAVFPDHAI AHGRPRFTAGPWKQAHATFYEGGSGTFFGGACGYHDVVQ
EGYGLETVALSNALFNNGQSCGACYDIKCVDQPQWCKPGSPILHATATNNCPPNWN
QASDNNGWCNPPREHFDAIKPVFLNIAEYKAGIVPVEYRRVPCQKKGGIRFTITGNPY
FNEVLVWNVAGAGDVSVQVKGKLNKLTMMKRMWQQRWVTDKLVGESLTFR
VLASDKRYSTSWHITPKNWQFGQTFEGKNFR*

CDS (coding sequence)

>PrpEXPA-03

ATGTTGGGTTTCATTGCTGCTCTTTCTTCTAGCAGTATTTCTGACCATGCCATTGCC
CACGGTAGGCCAAGGTTCACTGCTGGCCCTTGGAAGCAAGCTCATGCCACATTCT
ATGAAGGAGGCTCCGGAACATTTGGTGGAGCTTGCGGTTACCATGATGTTGTTCA
AGAAGGATATGGCCTGGAGACAGTAGCATTGAGCAATGCATTGTTCAACAACGG
ACAGTCATGTGGTGCATGCTACGATATCAAATGTGTAGACCAACCTCAATGGTGC
AAGCCCGGGAGTCCGATTCTGCATGCTACGGCAACTAACAATTGCCCCCGAATT
GGAATCAGGCAAGCGACAATGGAGGATGGTGCAATCCACCACGCGAGCATTTTG
ACATAGCTAAGCCTGTATTCTCAATATTGCCGAGTACAAGGCTGGAATCGTCCC
AGTCGAATACCGCAGGGTTCCATGCCAAAAGAAAGGAGGAATTCGATTTACGAT
AACCGGCAACCCTTACTTCAACGAAGTGTGGTTTGGAAATGTGGCAGGAGCTGGA
GATGTGGTCAGCGTGCAAGTGAAGGGCAACAAGTTGAAATGGACAATGATGAAG
AGGATGTGGGGTCAGAGGTGGGTTACTGATGCCAAGTTGGTTGGTGAGTCACTCA
CCTTCCGAGTCCTAGCAAGTGATAAACGATACTCCACTTCATGGCATATAACCCC
TAAGAATTGGCAGTTTGGCCAGACCTTCGAAGGCAAGA ACTTCCGATAG

Nucleotide

>PrpEXPA-03

ATGTTGGGTTTCATTGCTGCTCTTTCTTCTAGCAGTATTTCTGACCATGCCATTGCC
CACGGTAGGCCAAGGTTCACTGCTGGCCCTTGGAAGCAAGCTCATGCCACATTCT
ATGAAGGAGGCTCCGGAACATTTGGTATGAAATTCTAAAACAACGTCGTTTTGAA
CACGAGCACTATATTTTAGTTACATTATATATATATATTGAGCTTGTCAGGTGGAG
CTTGCGGTTACCATGATGTTGTTCAAGAAGGATATGGCCTGGAGACAGTAGCATT
GAGCAATGCATTGTTCAACAACGGACAGTCATGTGGTGCATGCTACGATATCAA

TGTGTAGACCAACCTCAATGGTGC AAGCCCGGGAGTCCGATTCTGCATGCTACGG
CAACTAACAATTGCCCGCCGAATTGGAATCAGGCAAGCGACAATGGAGGATGGT
GCAATCCACCACGCGAGCATTTTGACATAGCTAAGCCTGTATTCCTCAATATTGC
CGAGTACAAGGCTGGAATCGTCCCAGTCGAATACCGCAGGTAAATTTTCATGCATT
AATTCATGGACAATCTAATAACAACATAACATGTTGATAAAAGAGAATATTATCG
ATCGACCTTTTCATTATTATATATCATCATGTTCAACATTGAATGAAATCTCAATA
TGCTTTGCAGGGTTCCATGCCAAAAGAAAGGAGGAATTCGATTTACGATAACCGG
CAACCCTTACTTCAACGAAGTGTGGTTTGGGAATGTGGCAGGAGCTGGAGATGTG
GTCAGCGTGCAAGTGAAGGGCAACAAGTTGAAATGGACAATGATGAAGAGGATG
TGGGGTCAGAGGTGGGTACTGATGCCAAGTTGGTTGGTGAGTCACTCACCTTCC
GAGTCCTAGCAAGTGATAAACGATACTCCACTTCATGGCATATAACCCCTAAGAA
TTGGCAGTTTGGCCAGACCTTCGAAGGCAAGAACTTCCGATAG